

## FIG. 1A

GGATTGAACA AGGACGCATT TCCCCAGTAC ATCCACAAC ATG CTG TCC ACA TCT	54
Met Leu Ser Thr Ser	
1 5	
CGT TCT CGG TTT ATC AGA AAT ACC AAC GAG AGC GGT GAA GAA GTC ACC	102
Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser Gly Glu Glu Val Thr	
10 15 20	
ACC TTT TTT GAT TAT GAT TAC GGT GCT CCC TGT CAT AAA TTT GAC GTG	150
Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys His Lys Phe Asp Val	
25 30 35	
AAG CAA ATT GGG GCC CAA CTC CTG CCT CCG CTC TAC TCG CTG GTG TTC	198
Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe	
40 45 50	
ATC TTT GGT TTT GTG GGC AAC ATG CTG GTC GTC CTC ATC TTA ATA AAC	246
Ile Phe Gly Phe Val Gly Asn Met Leu Val Val Leu Ile Leu Ile Asn	
55 60 65	
TGC AAA AAG CTG AAG TGC TTG ACT GAC ATT TAC CTG CTC AAC CTG GCC	294
Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr Leu Leu Asn Leu Ala	
70 75 80 85	
ATC TCT GAT CTG CTT TTT CTT ATT ACT CTC CCA TTG TGG GCT CAC TCT	342
Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro Leu Trp Ala His Ser	
90 95 100	
GCT GCA AAT GAG TGG GTC TTT GGG AAT GCA ATG TGC AAA TTA TTC ACA	390
Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met Cys Lys Leu Phe Thr	
105 110 115	
GGG CTG TAT CAC ATC GGT TAT TTT GGC GGA ATC TTC TTC ATC ATC CTC	438
Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile Phe Phe Ile Ile Leu	
120 125 130	
CTG ACA ATC GAT AGA TAC CTG GCT ATT GTC CAT GCT GTG TTT GCT TTA	486
Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu	
135 140 145	

*FIG. 1B*

AAA GCC AGG ACG GTC ACC TTT GGG GTG GTG ACA AGT GTG ATC ACC TGG	534
Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp	
150 155 160 165	
TTG GTG GCT GTG TTT GCT TCT GTC CCA GGA ATC ATC TTT ACT AAA TGC	582
Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile Ile Phe Thr Lys Cys	
170 175 180	
CAG AAA GAA GAT TCT GTT TAT GTC TGT GGC CCT TAT TTT CCA CGA GGA	630
Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro Tyr Phe Pro Arg Gly	
185 190 195	
TGG AAT AAT TTC CAC ACA ATA ATG AGG AAC ATT TTG GGG CTG GTC CTG	678
Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile Leu Gly Leu Val Leu	
200 205 210	
CCG CTG CTC ATC ATG GTC ATC TGC TAC TCG GGA ATC CTG AAA ACC CTG	726
Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu	
215 220 225	
CTT CGG TGT CGA AAC GAG AAG AAG AGG CAT AGG GCA GTG AGA GTC ATC	774
Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Val Ile	
230 235 240 245	
TTC ACC ATC ATG ATT GTT TAC TTT CTC TTC TGG ACT CCC TAT AAC ATT	822
Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Thr Pro Tyr Asn Ile	
250 255 260	
GTC ATT CTC CTG AAC ACC TTC CAG GAA TTC TTC GGC CTG AGT AAC TGT	870
Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Ser Asn Cys	
265 270 275	
GAA AGC ACC AGT CAA CTG GAC CAA GCC ACG CAG GTG ACA GAG ACT CTT	918
Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln Val Thr Glu Thr Leu	
280 285 290	
GGG ATG ACT CAC TGC TGC ATC AAT CCC ATC ATC TAT GCC TTC GTT GGG	966
Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly	
295 300 305	

## FIG. 1C

GAG AAG TTC AGA AGC CTT TTT CAC ATA GCT CTT GGC TGT AGG ATT GCC	1014
Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu Gly Cys Arg Ile Ala	
310 315 320 325	
CCA CTC CAA AAA CCA GTG TGT GGA GGT CCA GGA GTG AGA CCA GGA AAG	1062
Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly Val Arg Pro Gly Lys	
330 335 340	
AAT GTG AAA GTG ACT ACA CAA GGA CTC CTC GAT GGT CGT GGA AAA GGA	1110
Asn Val Lys Val Thr Thr Gln Gly Leu Leu Asp Gly Arg Gly Lys Gly	
345 350 355	
AAG TCA ATT GGC AGA GCC CCT GAA GCC AGT CTT CAG GAC AAA GAA GGA	1158
Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu Gln Asp Lys Glu Gly	
360 365 370	
GCC TAGAGACAGA AATGACAGAT CTCTGCTTTG GAAATCACAC GTCTGGCTTC	1121
Ala	
ACAGATGTGT GATTCACAGT GTGAATCTTG GTGTCTACGT TACCAGGCAG GAAGGCTGAG	1271
AGGAGAGAGA CTCCAGCTGG GTTGGAAC AGTATTTTCC AAACCTACCTT CCAGTTCCTC	1331
ATTTTGAAT ACAGGCATAG AGTTCAGACT TTTTAAAT AGTAAAAATA AAATTAAGC	1391
TGAAACTGC AACTTGTAAG TGTGGTAAAG AGTTAGTTTG AGTTGCTATC ATGTCAAACG	1451
TGAAATGCT GTATTAGTCA CAGAGATAAT TCTAGCTTTG AGCTTAAGAA TTTTGAGCAG	1511
GTGGTATGTT TGGGAGACTG CTGAGTCAAC CCAATAGTTG TTGATTGGCA GGAGTTGGAA	1571
GTGTGTGATC TGTGGGCACA TTAGCCTATG TGCATGCAGC ATCTAAGTAA TGATGTCGTT	1631
TGAATCACAG TATACGCTCC ATCGCTGTCA TCTCAGCTGG ATCTCCATTC TCTCAGGCTT	1691
GCTGCCAAAA GCCTTTTGTG TTTTGTTTTG TATCATTATG AAGTCATGCG TTTAATCACA	1751
TTCGAGTGTT TCAGTGCTTC GCAGATGTCC TTGATGCTCA TATTGTTCCC TAATTTGCCA	1811
GTGGGAACTC CTAAATCAAA TTGGCTTCTA ATCAAAGCTT TTAAACCCTA TTGGTAAAGA	1871

*FIG. 1D*

ATGGAAGGTG GAGAAGCTCC CTGAAGTAAG CAAAGACTTT CCTCTTAGTC GAGCCAAGTT	1931
AAGAATGTTC TTATGTTGCC CAGTGTGTTT CTGATCTGAT GCAAGCAAGA AACACTGGGC	1991
TTCTAGAACC AGGCAACTTG GGAAGTAGAC TCCAAGCTG GACTATGGCT CTACTTTCAG	2051
GCCACATGGC TAAAGAAGGT TTCAGAAAGA AGTGGGGACA GAGCAGAACT TTCACCTTCA	2111
TATATTTGTA TGATCCTAAT GAATGCATAA AATGTTAAGT TGATGGTGAT GAAATGTAAA	2171
TACTGTTTTT AACAACTATG ATTTGGAAAA TAAATCAATG CTATAACTAT GTTGATAAAA	2231
G	2232

## FIG. 2A

CAGGACTGCC TGAGACAAGC CACAAGCTGA ACAGAGAAAG TGGATTGAAC AAGGACGCAT	60
TTCCCCAGTA CATCCACAAC ATG CTG TCC ACA TCT CGT TCT CGG TTT ATC	110
Met Leu Ser Thr Ser Arg Ser Arg Phe Ile	
1 5 10	
AGA AAT ACC AAC GAG AGC GGT GAA GAA GTC ACC ACC TTT TTT GAT TAT	158
Arg Asn Thr Asn Glu Ser Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr	
15 20 25	
GAT TAC GGT GCT CCC TGT CAT AAA TTT GAC GTG AAG CAA ATT GGG GCC	206
Asp Tyr Gly Ala Pro Cys His Lys Phe Asp Val Lys Gln Ile Gly Ala	
30 35 40	
CAA CTC CTG CCT CCG CTC TAC TCG CTG GTG TTC ATC TTT GGT TTT GTG	254
Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val	
45 50 55	
GGC AAC ATG CTG GTC GTC CTC ATC TTA ATA AAC TGC AAA AAG CTG AAG	302
Gly Asn Met Leu Val Val Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys	
60 65 70	
TGC TTG ACT GAC ATT TAC CTG CTC AAC CTG GCC ATC TCT GAT CTG CTT	350
Cys Leu Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu	
75 80 85 90	
TTT CTT ATT ACT CTC CCA TTG TGG GCT CAC TCT GCT GCA AAT GAG TGG	398
Phe Leu Ile Thr Leu Pro Leu Trp Ala His Ser Ala Ala Asn Glu Trp	
95 100 105	
GTC TTT GGG AAT GCA ATG TGC AAA TTA TTC ACA GGG CTG TAT CAC ATC	446
Val Phe Gly Asn Ala Met Cys Lys Leu Phe Thr Gly Leu Tyr His Ile	
110 115 120	
GGT TAT TTT GGC GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGA	494
Gly Tyr Phe Gly Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg	
125 130 135	
TAC CTG GCT ATT GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC	542
Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val	
140 145 150	

FIG. 2B

ACC TTT GGG GTG GTG ACA AGT GTG ATC ACC TGG TTG GTG GCT GTG TTT	590
Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp Leu Val Ala Val Phe	
155 160 165 170	
GCT TCT GTC CCA GGA ATC ATC TTT ACT AAA TGC CAG AAA GAA GAT TCT	638
Ala Ser Val Pro Gly Ile Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser	
175 180 185	
GTT TAT GTC TGT GGC CCT TAT TTT CCA CGA GGA TGG AAT AAT TTC CAC	686
Val Tyr Val Cys Gly Pro Tyr Phe Pro Arg Gly Trp Asn Asn Phe His	
190 195 200	
ACA ATA ATG AGG AAC ATT TTG GGG CTG GTC CTG CCG CTG CTC ATC ATG	734
Thr Ile Met Arg Asn Ile Leu Gly Leu Val Leu Pro Leu Leu Ile Met	
205 210 215	
GTC ATC TGC TAC TCG GGA ATC CTG AAA ACC CTG CTT CGG TGT CGA AAC	782
Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn	
220 225 230	
GAG AAG AAG AGG CAT AGG GCA GTG AGA GTC ATC TTC ACC ATC ATG ATT	830
Glu Lys Lys Arg His Arg Ala Val Arg Val Ile Phe Thr Ile Met Ile	
235 240 245 250	
GTT TAC TTT CTC TTC TGG ACT CCC TAT AAC ATT GTC ATT CTC CTG AAC	878
Val Tyr Phe Leu Phe Trp Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn	
255 260 265	
ACC TTC CAG GAA TTC TTC GGC CTG AGT AAC TGT GAA AGC ACC AGT CAA	926
Thr Phe Gln Glu Phe Phe Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln	
270 275 280	
CTG GAC CAA GCC ACG CAG GTG ACA GAG ACT CTT GGG ATG ACT CAC TGC	974
Leu Asp Gln Ala Thr Gln Val Thr Glu Thr Leu Gly Met Thr His Cys	
285 290 295	
TGC ATC AAT CCC ATC ATC TAT GCC TTC GTT GGG GAG AAG TTC AGA AGG	1022
Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe Arg Arg	
300 305 310	

## FIG. 2C

TAT CTC TCG GTG TTC TTC CGA AAG CAC ATC ACC AAG CGC TTC TGC AAA	1070
Tyr Leu Ser Val Phe Phe Arg Lys His Ile Thr Lys Arg Phe Cys Lys	
315 320 325 330	
CAA TGT CCA GTT TTC TAC AGG GAG ACA GTG GAT GGA GTG ACT TCA ACA	1118
Gln Cys Pro Val Phe Tyr Arg Glu Thr Val Asp Gly Val Thr Ser Thr	
335 340 345	
AAC ACG CCT TCC ACT GGG GAG CAG GAA GTC TCG GCT GGT TTA	1160
Asn Thr Pro Ser Thr Gly Glu Gln Glu Val Ser Ala Gly Leu	
350 355 360	
TAAAACGAGG AGCAGTTTGA TTGTTGTTTA TAAAGGGAGA TAACAATCTG TATATAACAA	1220
CAAACTTCAA GGGTTTGTTG AACAATAGAA ACCTGTAAAG CAGGTGCCCA GGAACCTCAG	1280
GGCTGTGTGT ACTAATACAG ACTATGTCAC CCAATGCATA TCCAACATGT GCTCAGGGAA	1340
TAATCCAGAA AAAGTGTGGG TAGAGACTTT GACTCTCCAG AAAGCTCATC TCAGCTCCTG	1400
AAAAATGCCT CATTACCTTG TGCTAATCCT CTTTTTCTAG TCTTCATAAT TTCTTCACTC	1460
AATCTCTGAT TCTGTCAATG TCTTGAAATC AAGGGCCAGC TGGAGGTGAA GAAGAGAATG	1520
TGACAGGCAC AGATGAATGG GAGTGAGGGA TAGTGGGGTC AGGGCTGAGA GGAGAAGGAG	1580
GGAGACATGA GCATGGCTGA GCCTGGACAA AGACAAAGGT GAGCAAAGGG CTCACGCATT	1640
CAGCCAGGAG ATGATACTGG TCCTTAGCCC CATCTGCCAC GTGTATTTAA CCTTGAAGGG	1700
TTCACCAGGT CAGGGAGAGT TTGGGAACTG CAATAACCTG GGAGTTTTGG TGGAGTCCGA	1760
TGATTCTCTT TTGCATAAGT GCATGACATA TTTTGTCTT ATTACAGTTT ATCTATGGCA	1820
CCCATGCACC TTACATTTGA AATCTATGAA ATATCATGCT CCATTGTTCA GATGCTTCTT	1880
AGGCCACATC CCCCTGTCTA AAAATTCAGA AAATTTTGT TTATAAAAGA TGCATTATCT	1940
ATGATATGCT AATATATGTA TATGCAATAT AAAATTTAG	1979

FIG. 3(A)

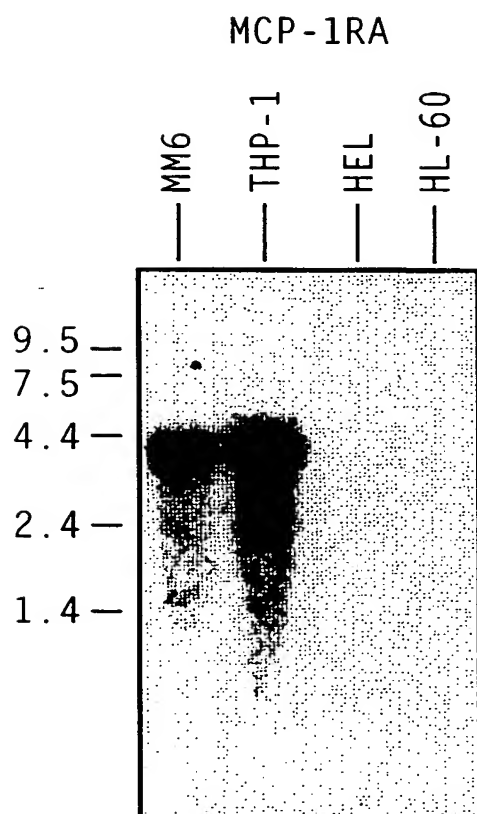


FIG. 3(B)

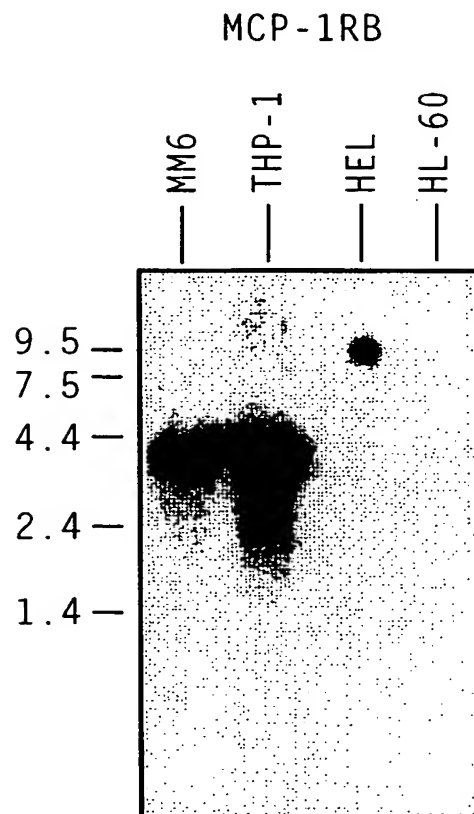


FIG.4(A)

MCP-1RA (CCR2-A)	MLSTSRSRFIRNTNESGEEVTTFDYDYG--APCHKFDVKQIGAQLLPPL	48
MIP-1 $\alpha$ /RANTESR	M-----ETPNTTEDYDTTTFDYGDATPCQKVNERAFGAQLLPPL	40
HUMSTR	MEGIS---IYTSNYTEEMGS-GDYDSMK-EPCFREENANFNKIFLPTI	44
IL-8RA	MSNITDPQ-MWDFDDLNFTGMPPADEDY---SPC-MLETETLNKYVVIIA	45
IL-8RB	MESDSFEDFWKGEDLSNYSYSTLPFFLLDAAPC-EPESLEINKYFVVII	49
	<u>48</u> <u>1</u> <u>69</u> <u>79</u> <u>2</u>	
MCP-1RA (CCR2-A)	YSLVFIIFGFVGNMLVVLIIINCKKLKCLTDIYLLNLAISDLLFLITLPLW	98
MIP-1 $\alpha$ /RANTESR	YSLVFVIGLVGNILVVLVIVQYKRLKNMTSIYLLNLAISDLLFLITLPLW	90
HUMSTR	YSITIFLTGIVGNGLVILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPLW	94
IL-8RA	YALVFLLSLLGNSLVMVILYSRVGRSVTDVYLLNLALADLLFALTLPW	95
IL-8RB	YALVFLLSLLGNSLVMVILYSRVGRSVTDVYLLNLALADLLFALTLPW	99
	<u>101</u> <u>115</u> <u>3</u> <u>136</u>	
MCP-1RA (CCR2-A)	AH-SAAENEVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIVHAVF	147
MIP-1 $\alpha$ /RANTESR	IDYKLKDDVFGDAMCKILSGFYITGLYSEIFFIILLTIDRYLAIVHAVF	140
HUMSTR	AV-DAVANWYFGNFLCKAVHVIYTVNLYSSVLILAFISLDRYLAIVHATN	143
IL-8RA	AA-SKVNQWIFGTFLCKVVSLLKEVNFYSGITLLACISVDRYLAIVHATR	144
IL-8RB	AA-SKVNQWIFGTFLCKVVSLLKEVNFYSGITLLACISVDRYLAIVHATR	148
	<u>154</u> <u>4</u> <u>178</u>	
MCP-1RA (CCR2-A)	ALKARTVTFGVVTSVITLVAVFASVPGIIFTKCKEDSVYVCGPYFP--	195
MIP-1 $\alpha$ /RANTESR	ALRARTVTFGVITSIIIALAILASMPGLYFSKTQWEFTHTCSLHFPHE	190
HUMSTR	SQRPRKLLAEKVYVGVWIPALLTIPDFIFANVSEADDRYICDRFYPN-	192
IL-8RA	TLTQKR-HLVKFVCLGCWGLSMNLSLPFFLFRQAYHPNNSSPVCYEV LGN	193
IL-8RB	TLTQKRYLVKFI-CLSIWGLSLLLALPVLLFRRTVYSSNVSPACYEDMGN	197
	<u>204</u> <u>5</u> <u>231</u>	
MCP-1RA (CCR2-A)	--RGWNNFHTIMRNILGLVLP LLIMVICYS GILKTLLRCRNEKKRHRAVR	243
MIP-1 $\alpha$ /RANTESR	SLREWKLFOALKNLFGVLVPLLVMITCYTGIIKILLRRPNEKKS-KAVR	239
HUMSTR	--DLWVVVFQFQHIMVGLILPGIVILFCYCIISKLSHSGKHQKR-KALK	239
IL-8RA	DTAKWRMVLRIPLHTFGFIVPLFVMLFCYGT LRTL FKAHMGQK-HRAMR	242
IL-8RB	NTANWRMLLRILPQSFGFIVPLLIMLFCYGT LRTL FKAHMGQ-KHRAMR	246
	<u>244</u> <u>6</u> <u>268</u>	
MCP-1RA (CCR2-A)	VIFTIMIVYFLFWTPYNIIVILLNTFQEF-FGLSNCESTSQ LDOATQVTET	292
MIP-1 $\alpha$ /RANTESR	LIFVIMIIFFLFWTPYNLTILISVFQDF-LFTHCEQSRHLDLAVQVTEV	288
HUMSTR	TTVILILAFFACWLPYYIGISIDSFILLEIKQGEFENTVHKWISITEA	289
IL-8RA	VIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNNIGRALDATEI	292
IL-8RB	VIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDATEI	296

FIG. 4(B)

	295	7	313	
MCP-1RA (CCR2-A)	LGMTHCCINPIIYAFVGEKFRSL*	FHIALGCRIAPLQKPVCGGPGV	VRPGKN	342
MIP-1 $\alpha$ /RANTESR	IAYTHCCVNPVIYAFVGERFRKYL	RQLFHRVA	-----VHLVKW	327
HUMSTSR	LAFHCCLNPIIYAFLGAKFKTSAQ	HALTS	-----VSRGSS	325
IL-8RA	LGFLHSCLNPIIYAFIQNFRHG	FLKILA	-----MHGLVS	327
IL-8RB	LGILHSCLNPLIYAFIQKFRH	GLLKILAIH	-----GLIS	331
MCP-1RA (CCR2-A)	VKVTTQGLLDGRGKGKSIGRAPEAS	LQDKEGA		374
MIP-1 $\alpha$ /RANTESR	LPFLSVDRLE-RVSSTS-PSTGEHEL	--SAGF		355
HUMSTSR	LKILSKGK---RGGHSSVSTESESS	--FHSS		352
IL-8RA	KEFLARH---RVTSYT-SSSVNVS	----SNL		350
IL-8RB	KDSLPKDS---RPSFVG-SSSGHTS	----TTL		355

FIG. 5

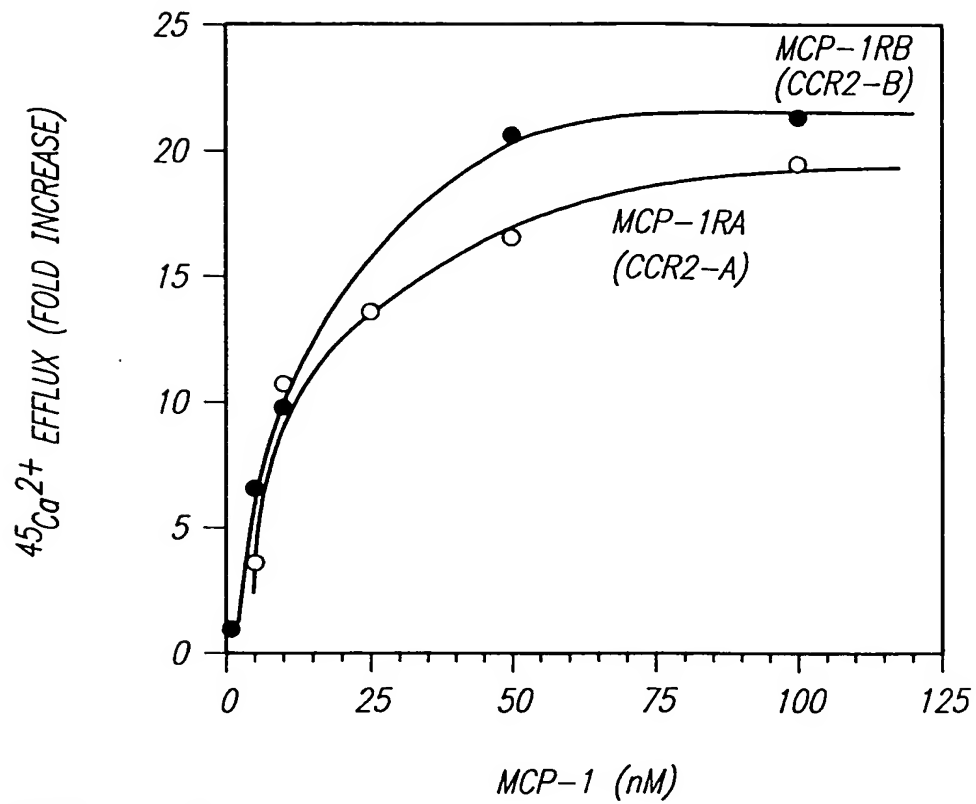
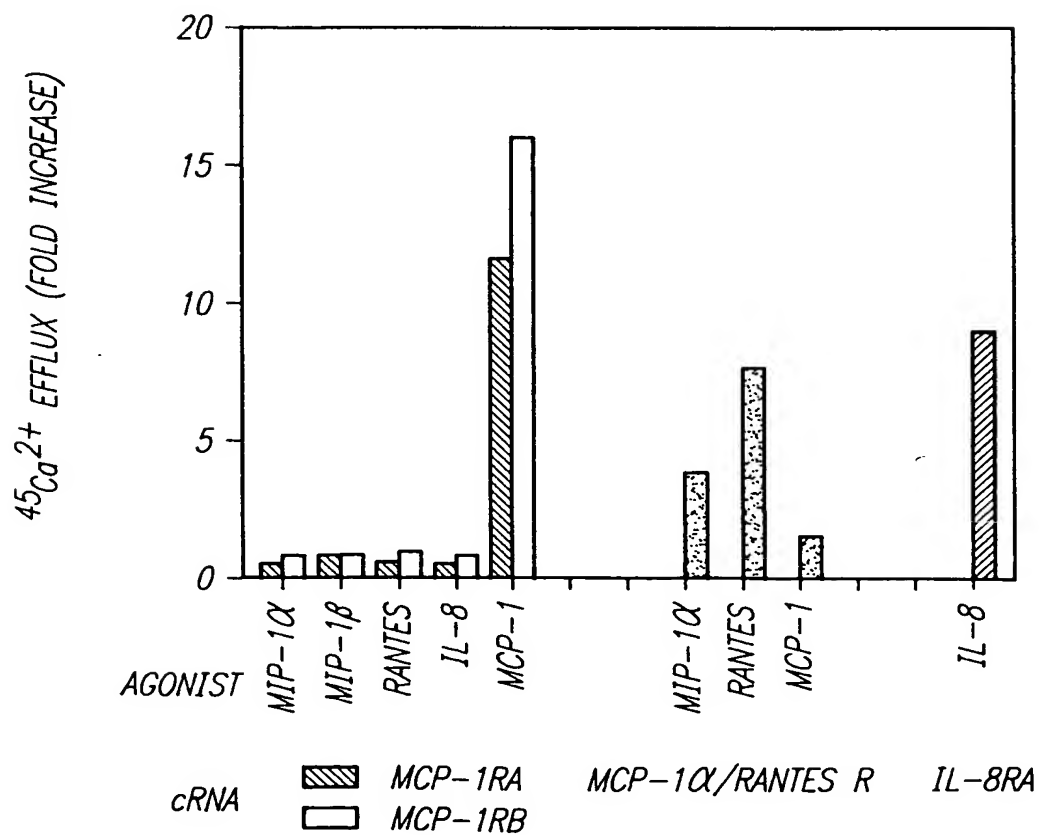


FIG. 6



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FIG. 7A

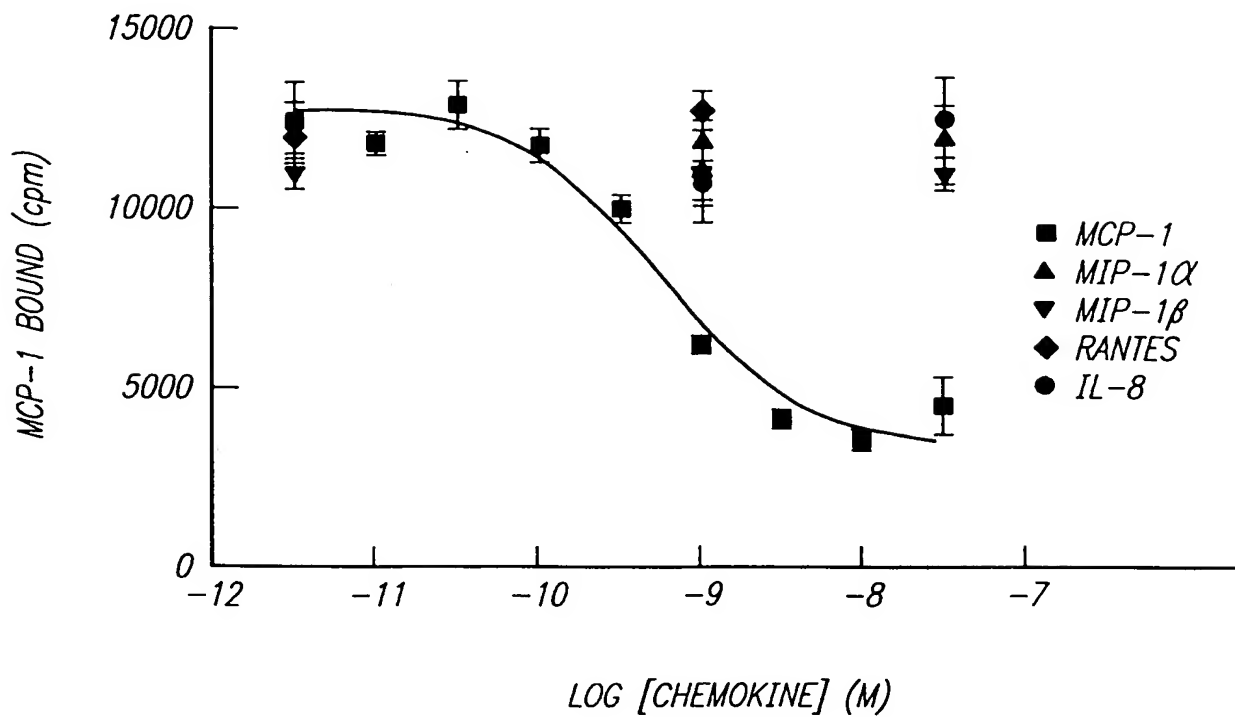
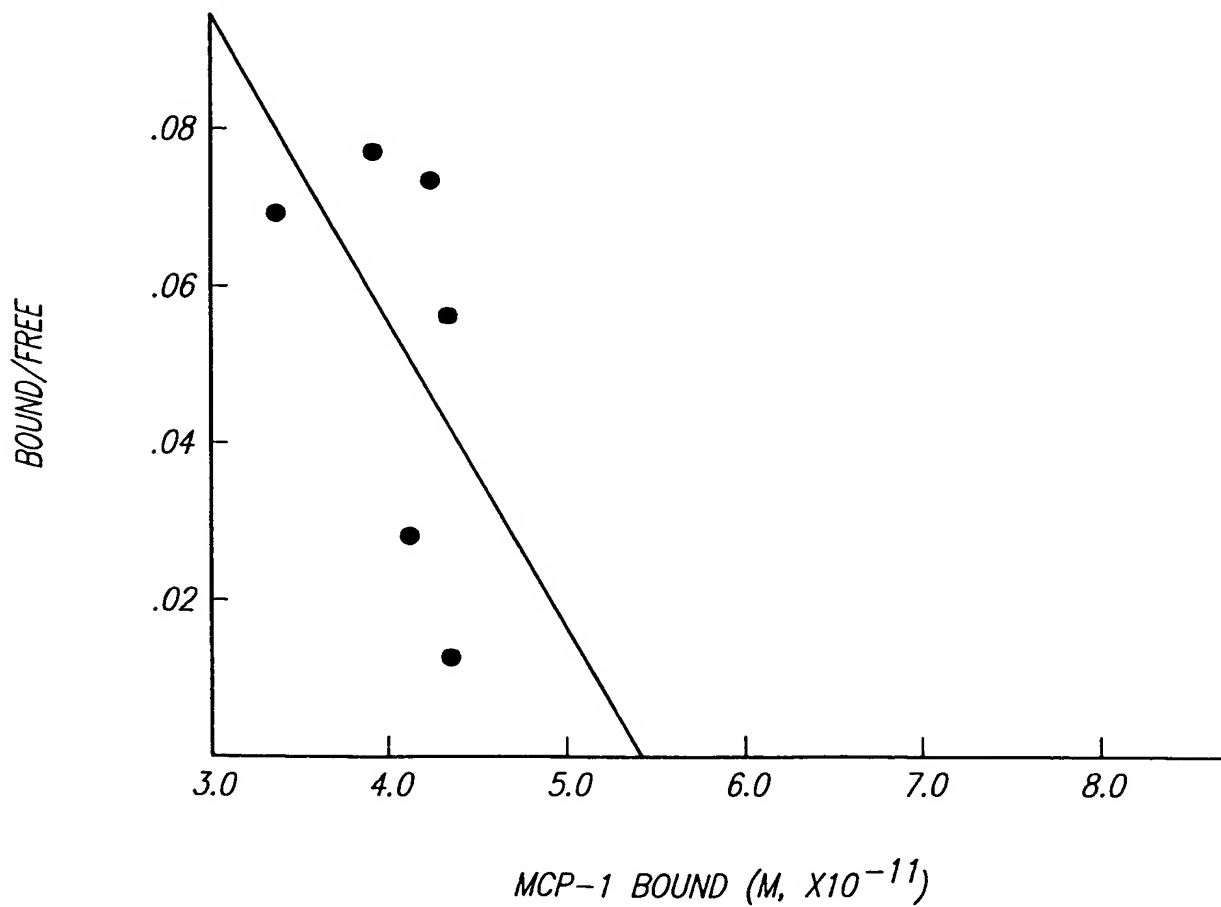


FIG. 7B



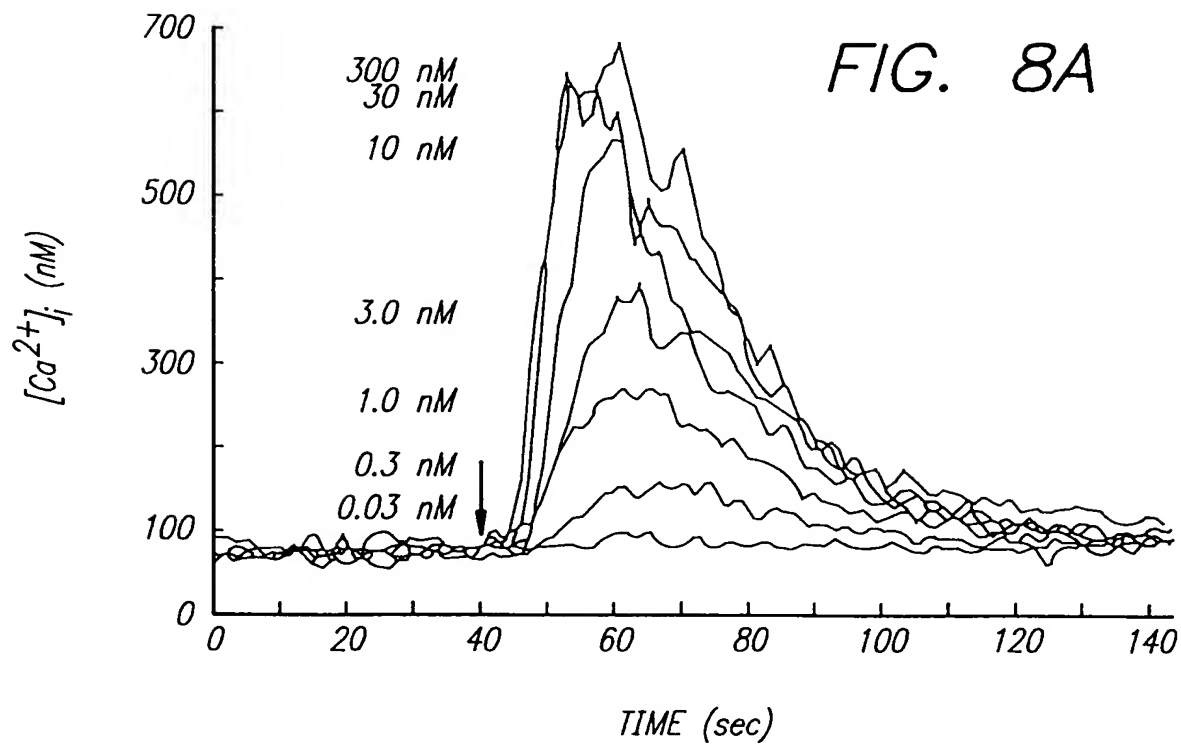
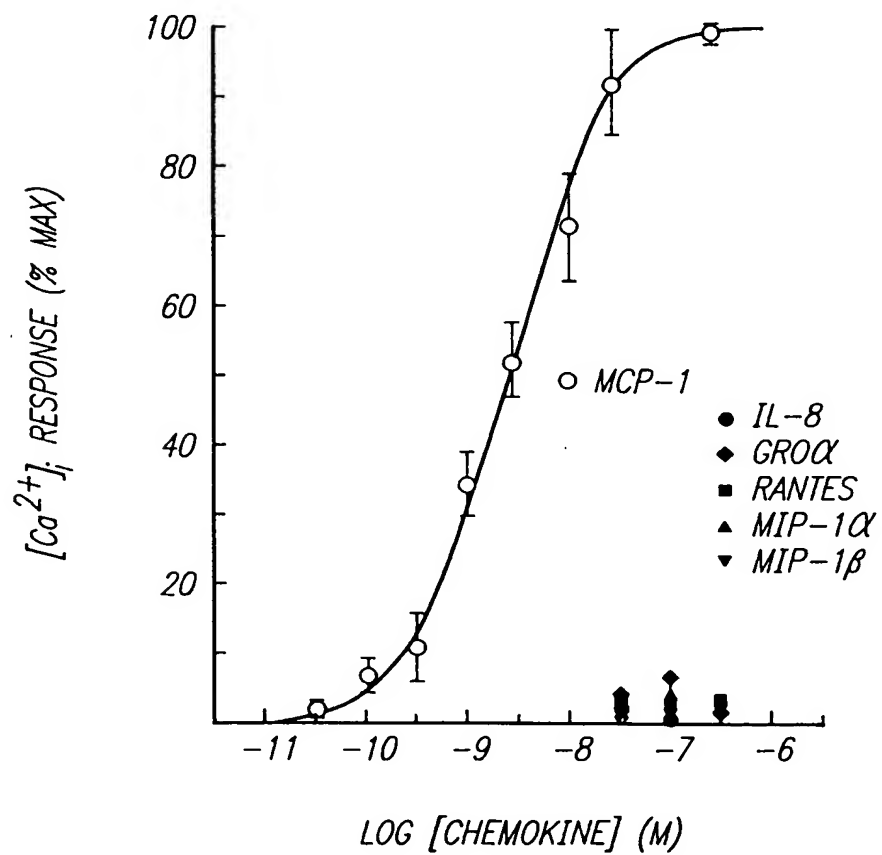
**FIG. 8B**

FIG. 8C

